

1632

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/724,693A

DATE: 02/06/2001
 TIME: 16:04:47

Input Set : A:\402gseq.002
 Output Set: N:\CRF3\02062001\I724693A.raw

SEQUENCE LISTING

C--> 4 (1) GENERAL INFORMATION:
 6 (i) APPLICANT: Hadlaczky, Gyula
 7 Szalay, Aladar
 C--> 9 (ii) TITLE OF INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
 10 AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
 12 (iii) NUMBER OF SEQUENCES: 34
 14 (iv) CORRESPONDENCE ADDRESS:
 15 (A) ADDRESSEE: Heller Ehrman White & McAuliffe
 16 (B) STREET: 4250 Executive Square, 7th Floor
 17 (C) CITY: La Jolla
 18 (D) STATE: CA
 19 (E) COUNTRY: USA
 20 (F) ZIP: 92037
 22 (v) COMPUTER READABLE FORM:
 23 (A) MEDIUM TYPE: Diskette
 24 (B) COMPUTER: IBM Compatible
 25 (C) OPERATING SYSTEM: DOS
 26 (D) SOFTWARE: FastSEQ Version 1.5
 28 (vi) CURRENT APPLICATION DATA:
 C--> 29 (A) APPLICATION NUMBER: US/09/724,693A
 C--> 30 (B) FILING DATE: 28-Nov-2000
 50 (C) CLASSIFICATION:
 C--> 47 (vii) PRIOR APPLICATION DATA:
 33 (A) APPLICATION NUMBER: 08/835,682
 34 (B) FILING DATE: 10-APR-1997
 38 (A) APPLICATION NUMBER: 08/695,191
 39 (B) FILING DATE: 07-AUG-1996
 43 (A) APPLICATION NUMBER: 08/682,080
 44 (B) FILING DATE: 15-JUL-1996
 48 (A) APPLICATION NUMBER: 08/629,822
 49 (B) FILING DATE: 10-APR-1996
 52 (viii) ATTORNEY/AGENT INFORMATION:
 53 (A) NAME: Seidman, Stephanie L
 54 (B) REGISTRATION NUMBER: 33,779
 55 (C) REFERENCE/DOCKET NUMBER: 24601-402G
 58 (ix) TELECOMMUNICATION INFORMATION:
 59 (A) TELEPHONE: 858-450-8403
 60 (B) TELEFAX: 858-587-5360
 61 (C) TELEX:
 63 (2) INFORMATION FOR SEQ ID NO: 1:
 65 (i) SEQUENCE CHARACTERISTICS:
 66 (A) LENGTH: 1293 base pairs
 67 (B) TYPE: nucleic acid
 68 (C) STRANDEDNESS: single
 69 (D) TOPOLOGY: linear
 71 (ii) MOLECULE TYPE: Genomic DNA

Does Not Comply
 Corrected Diskette Needed

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FEB 20 2001

TECH CENTER 1600/2900

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72      (iii) HYPOTHETICAL: NO
C--> 73      (iv) ANTI-SENSE: NO
W--> 74      (v) FRAGMENT TYPE:
75      (vi) ORIGINAL SOURCE:
76      (ix) FEATURE:
78      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
80  GAATTCATCA TTTTTCANGT CCTCAAGTGG ATGTTTCTCA TTTNCCATGA TTTTAAGTTT      60
81  TCTCGCCATA TTCTGGTCC TACAGTGTGC ATTTCTCCAT TTTNCACGTT TTNCAGTGAT      120
82  TTCGTCAATT TCAAGTCCTC AAGTGGATGT TTCTCATTTN CCATGAATTT CAGTTTCTCN      180
83  GCCATATTCC ACGTCCTACA GNGGACATTT CTAAATTTNC CACCTTTTTC AGTTTTCCTC      240
84  GCCATATTTC ACGTCCTAAA ATGTGTATTT CTCGTTTNC GTGATTTTCA GTTTTCTCGC      300
85  CAGATTCCAG GTCTATAAT GTGCATTTCT CATTNNCAC GPTTTTCAGT GATTTCGTCA      360
86  TTTTTCGAAG TCGGCAAGTG GATGTTTCTC ATTTNCCATG ATTTNCAGTT TTCTTGNAAT      420
87  ATTCCATGTC CTACAATGAT CATTTTAAAT TTTCCACCTT TTCATTTTTC CACGCCATAT      480
88  TTCATGTCCT AAAGTGTATA TTTCTCCTTT TCCGCGATTT TCAGTTTCTC CGCCATATTC      540
89  CAGGTCCTAC AGTGTGCATT CCTCATTTT CACCTTTTTC ACTGATTTTCG TCATTTTTC      600
90  AGTCGTCAAC TGGATCTTTC TAATTTTCCA TGATTTTCAG TTATCTTGTC ATATTCCATG      660
91  TCCTACAGTG GACATTTCTA AATTTTCCAA CTTTTCATAT TTTTCTCGAC ATATTGACG      720
92  TGCTAAAGTG TGTATTTCTT ATTTTCCGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGTC      780
93  CTAATAGTGT GCATTTCTCA TTTTCCAGT TTTTCAGTGA TTTCTGCATT TTTTCCAGTT      840
94  GTCAAGGGGA TGTTCCTCAT TTTCCATGAG TGTAGTTTTC CTTGCTATAT TCCATGTCCT      900
95  ACAGTGACAT TTCTAAATAT TATACCTTTT TCAGTTTTC TCACCATATT TCACGTCCTA      960
96  AAGTATATAT TTCTCATTTT CCTGATTTT CAGTTTCTT GCCATATTCC AGGTCCTACA      1020
97  GTGTGCATTT CTCATTTTTC ACGTTTTC TAATTTTCTT CATTTTAA GCGCTCAAAT      1080
98  GGATGTTTCT CATTTTCCAT GATTTCAGT TTTCTTGCCA TATACCATGT CCTACAGTGG      1140
99  ACATTTCTAA ATTATCCACC TTTTTCAGTT TTTTCATCGGC ACATTTACAG TCCTAAAGTG      1200
100  TGTATTTCTA ATTTTCAGTG ATTTTCAGTT TTCTCGCCAT ATTCCAGGAC CTACAGTGTG      1260
101  CATTCTCAT TTTTCACGTT TTTTCAGTGA TTC      1293
103 (2) INFORMATION FOR SEQ ID NO: 2:
105      (i) SEQUENCE CHARACTERISTICS:
106          (A) LENGTH: 1044 base pairs
107          (B) TYPE: nucleic acid
108          (C) STRANDEDNESS: single
109          (D) TOPOLOGY: linear
111      (ii) MOLECULE TYPE: Genomic DNA
112      (iii) HYPOTHETICAL: NO
C--> 113      (iv) ANTI-SENSE: NO
W--> 114      (v) FRAGMENT TYPE:
115      (vi) ORIGINAL SOURCE:
116      (ix) FEATURE:
118      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
120  AGGCCTATGG TGAAAAAGGA AATATCTTCC CCTGAAAAC AGACAGAAGG ATTCTCAGAA      60
121  TCTTATTTGT GATGTGCGCC CCTCAACTAA CAGTGTGAA GCTTTCTTTT GATAGAGCAG      120
122  TTTTGAAACA CTCTTTTGT AAAATCTGCA AGAGGATATT TGGATAGCTT TGAGGATTTT      180
123  CGTTGGAAAC GGGATTGTCT TCATATAAAC CCTAGACAGA AGCATTCTCA GAAGCTTCAT      240
124  TGGGATGTTT CAGTTGAAGT CACAGTGTG AACAGTCCCC TTTCATAGAG CAGGTTTGAA      300
125  ACACTCTTTT TTGTAGTATC TGGAAGTGGA CATTTGGAGC GATCTCAGGA CTGCGGTGAA      360
126  AAAGGAAATA TCTTCCAATA AAAGCTAGAT AGAGGCAATG TCAGAAACCT TTTTCATGAT      420
127  GTATCTACTC AGCTAACAGA GTTGAACCTT CCTTTGAGAG AGCAGTTTGT AAACACTCTT      480

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128 TTGTGGAAT CTGCAAGTGG ATATTGTCT AGCTTTGAGG ATTTCTGTGG GAAACGGGAT 540
129 TACATATAAA AAGCAGACAG CAGCATTCCC AGAAACTTCT TTGTGATGTT TGCATTCAAG 600
130 TCACAGAGTT GAACATTCCC TTTCATAGAG CAGGTTTGAA ACACACTTTT TGAATGATCT 660
131 GGATGTGGAC ATTTGCAGCG CTTTCAGGCC TAAGGTGAAA AGGAAATATC TTCCCCTGAA 720
132 AACTAGACAG AAGCATTCTC AGAAACTTAT TTGTGATGTG CGCCCTCAAC TAACAGTGT 780
133 GAAGCTTTCT TTTCATAGAG GCAGTTTGA AACACTCTTT TGTGGAATCT GCAAGTGGAT 840
134 ATTTGTCTAG CTTTGAGGAT TTCTTTGGAA ACGGGATTAC ATATAAAAAG CAGACAGCAG 900
135 CATTTCCAGA ATCTTGTGTT TGAATGTTGC ATTCAAGTCA CAGAGTTGAA CATTCCTTT 960
136 CAGAGAGCAG GTTTGAACAC TCTTTTATA GTATCTGGAT GTGGACATTT GGAGCGCTTT 1020
137 CAGGGGGGAT CCTCTAGAAT TCCT 1044

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141 (2) INFORMATION FOR SEQ ID NO: 3:

143 (i) SEQUENCE CHARACTERISTICS:

144 (A) LENGTH: 2492 base pairs

145 (B) TYPE: nucleic acid

146 (C) STRANDEDNESS: single

147 (D) TOPOLOGY: linear

149 (ii) MOLECULE TYPE: Genomic DNA

150 (iii) HYPOTHETICAL: NO

C--> 151 (iv) ANTI-SENSE: NO

W--> 152 (v) FRAGMENT TYPE:

153 (vi) ORIGINAL SOURCE:

154 (ix) FEATURE:

156 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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158 CTGCAGCTGG GGGTCTCCAA TCAGGCAGGG GCCCTTACT ACTCAGATGG GGTGGCCGAG 60
159 TAGGGGAAGG GGGTGCAGGC TGCATGAGTG GACACAGCTG TAGGACTACC TGGGGGCTGT 120
160 GGATCTATGG GGGTGGGGAG AAGCCCAGTG ACAGTGCCTA GAAGAGACAA GGTGGCCTGA 180
161 GAGGTCTCA GGAACATAGA GCTGGCCATG TTGGGGCCAG GTCTCAAGCA GGAAGTGAGG 240
162 AATGGGACAG GCTTGAGGAT ACTCTACTCA GTAGCCAGGA TAGCAAGGAG GGCTTGGGGT 300
163 TGCTATCCTG GGGTCAACC CCCCAGGTTG AAGGCCCTGG GGGAGATGGT CCCAGGACAT 360
164 ATTACAATGG ACACAGGAGG TTGGGACACC TGGAGTCACC AAACAAACC ATGCCAAGAG 420
165 AGACCATGAG TAGGGGTGTC CAGTCCAGCC CTCTGACTGA GCTGCATTGT TCAAAATCCAA 480
166 AGGGCCCTG CTGCCACCTA GTGGCTGATG GCATCCACAT GACCCTGGGC CACACGCGTT 540
167 TAGGGTCTCT GTGAAGACCA AGATCCTTGT TACATTGAAC GACTCCTAAA TGAGCAGAGA 600
168 TTTCACCTA TTCGAAACAA TCACATAAAA TCCATCCTGG AAAAAGCCTG GGGGATGCCA 660
169 CTAAGGCTAG GGATAGGGTG GGATGAAGAT TATAGTTACA GTAAGGGGTT TAGGGTTAGG 720
170 GATCAACGTT GGTAGGAGT TAGGGATACA GTAGGGTACC GGTAGGGTTA GGGCTTAGGG 780
171 TTAGGGGTTA GGGTTAGGGT TAGGGTTAGG GTTAGGGTTA GGGGTAGGG GTTAGGGTTA 840
172 GGGTTAGGTT TTGGGGTGGC GTATTTTGGT CTATACGCT GTGTCCACT GGCAATGAAA 900
173 AGAGTTCTTG TTTTCTCTC AGCAATTTGT CATTTTAAA AGAGTTTAGC AATCTAACA 960
174 GATATAGACC AGCTGTGCTA TCTCATTTGT GTTTTCAATT GTAACCACAT TGTGGTTTCA 1020
175 ATGTGTTTAC TTGCCATCTG TAGATCTTCT TTGCGTGAGG TGTCTGTTCA GATGTGTGTG 1080
176 CATTTCTTGN NTTTNGGCTG TTAACTTAT TGTTTAGTTT TAATAATTTT TTATATATTT 1140
177 GAAGACAAAT CTTTCTCAGA TGTGTATTTG CAAATATTTT TTCAATATGA GGCTTGCTTT 1200
178 TGTCTCTAAC AAGGTCTCTT CAGAGATAAC TTAAATATAA GAAATCCACA CTGTCACTTC 1260
179 TTTTGTGTAT ATCTACCTTT TGTGTCATTT GTTAAATTC ATTACCAAAC CCAAAGGCAG 1320
180 ATAGCTTTTC TTCTATTGTT TCTTCTAGAA ATTTGTATAG TTTTGCATTT TTAGTGTAAG 1380
181 GATGATTTTG AGTGATTATT TGTGTAAGTT GTAAAGTTT CGTCTATATC CATATCATTT 1440
182 CTTATGGTTT CCAATTAATC GTTCCCTCAC TATTTTGGG AAAGACACAG GATAGTGGGC 1500
183 TTTGTTAGAG TAGATAGGTA GCTAGACATG AACAGGAGGG GGCCTCCTGG AAAAGGGAAA 1560

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184 GTCTGGGAAG GCTCACCTGG AGGACCACCA AAAATTACACA TATTAGTAGC ATCTCTAGTG 1620
185 CTGGAGTGGA TGGGCACTTG TCAATTGTGG GTAGGAGGCA AAAGAGGTCC TATGCAGAAA 1680
186 GAAACTCCCT AGAACTCCTC TGAAGATGCC CCAATCATTC ACTCTGCAAT AAAAATGTCA 1740
187 GAATATTGCT AGCTACATGC TGATAAGGNN AAAGGGGACA TTCTTAAGTG AAACCTGGCA 1800
188 CCATAAGTAC ACATTAGGGC AGAGAAGGAC ATTCAAAAGA GGCAGGCGCA GTAGGTACAA 1860
189 ACGTGATCGC TGTCAGTGTG CCTGGGATGG CGGGAAGGAG GCTGGTGCCA GAGTGGATTC 1920
190 GTATTGATCA CCACACATAT ACCTCAACCA ACAGTGAGGA GGTCCCACAA GCCTAAGTGG 1980
191 GGCAAGTTGG GGAGCTAAGG CAGTAGCAGG AAAACCAGAC AAAGAAAACA GGTGGAGACT 2040
192 TGAGACAGAG GCAGGAATGT GAAGAAATCC AAAATAAAAT TCCCTGCACA GGACTCTTAG 2100
193 GCTGTTTAAT GCATCGCTCA GTCCCACTCC TCCCTATTTT TCTACAATAA ACTCTTTACA 2160
194 CTCTGTTTCT TTTCAATGAA GTTATCTGCC ATCTTTGTAT TGCCTCTTGG TGAAAATGTT 2220
195 TCTTCCAAGT TAAACAAGAA CTGGGACATC AGCTCTCCCC AGTAATAGCT CCGTTTCAGT 2280
196 TTGAATTAC AGAACTGATG GGCTTAATAA CTGGCGCTCT GACTTTAGTG GTGCAGGAGG 2340
197 CCGTCACACC GGGACCAAGA GTGCCCTGCC TAGTCCCCAT CTGCCCCGAG GTGGCGGCTG 2400
198 CCTCGACACT GACAGCAATA GGGTCCGGCA GTGTCCCCAG CTGCCAGCAG GGGGCGTACG 2460
199 ACGACTACAC TGTGAGCAAG AGGGCCCTGC AG 2492
201 (2) INFORMATION FOR SEQ ID NO: 4:
203 (i) SEQUENCE CHARACTERISTICS:
204 (A) LENGTH: 28 base pairs
205 (B) TYPE: nucleic acid
206 (C) STRANDEDNESS: single
207 (D) TOPOLOGY: linear
209 (ii) MOLECULE TYPE: Genomic DNA
210 (iii) HYPOTHETICAL: NO
C--> 211 (iv) ANTI-SENSE: NO
W--> 212 (v) FRAGMENT TYPE:
213 (vi) ORIGINAL SOURCE:
214 (ix) FEATURE:
216 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
218 GGGGAATTCA TTGGGATGTT TCAGTTGA 28
220 (2) INFORMATION FOR SEQ ID NO: 5:
222 (i) SEQUENCE CHARACTERISTICS:
223 (A) LENGTH: 29 base pairs
224 (B) TYPE: nucleic acid
225 (C) STRANDEDNESS: single
226 (D) TOPOLOGY: linear
228 (ii) MOLECULE TYPE: Genomic DNA
229 (iii) HYPOTHETICAL: NO
C--> 230 (iv) ANTI-SENSE: NO
W--> 231 (v) FRAGMENT TYPE:
232 (vi) ORIGINAL SOURCE:
233 (ix) FEATURE:
235 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
237 CGAAAGTCCC CCCTAGGAGA TCTTAAGGA 29
239 (2) INFORMATION FOR SEQ ID NO: 6:
241 (i) SEQUENCE CHARACTERISTICS:
242 (A) LENGTH: 47 base pairs
243 (B) TYPE: nucleic acid
244 (C) STRANDEDNESS: single

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 PATENT APPLICATION: US/09/724,693A
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245          (D) TOPOLOGY: linear
W--> 247      (ii) MOLECULE TYPE: DNA
248          (iii) HYPOTHETICAL: NO
C--> 249      (iv) ANTI-SENSE: NO
W--> 250      (v) FRAGMENT TYPE:
251          (vi) ORIGINAL SOURCE:
252          (ix) FEATURE:
254          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
256 CCGCTTAATA CTCGTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC 47
260 (2) INFORMATION FOR SEQ ID NO: 7:
262          (i) SEQUENCE CHARACTERISTICS:
263              (A) LENGTH: 25 base pairs
264              (B) TYPE: nucleic acid
265              (C) STRANDEDNESS: single
266              (D) TOPOLOGY: linear
268          (ii) MOLECULE TYPE: Genomic DNA
269          (iii) HYPOTHETICAL: NO
C--> 270      (iv) ANTI-SENSE: NO
W--> 271      (v) FRAGMENT TYPE:
272          (vi) ORIGINAL SOURCE:
273          (ix) FEATURE:
275          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
277 CGATTTAAT TAATTAAGCC CGGGC 25
280 (2) INFORMATION FOR SEQ ID NO: 8:
282          (i) SEQUENCE CHARACTERISTICS:
283              (A) LENGTH: 27 base pairs
284              (B) TYPE: nucleic acid
285              (C) STRANDEDNESS: single
286              (D) TOPOLOGY: linear
288          (ii) MOLECULE TYPE: Genomic DNA
289          (iii) HYPOTHETICAL: NO
C--> 290      (iv) ANTI-SENSE: NO
W--> 291      (v) FRAGMENT TYPE:
292          (vi) ORIGINAL SOURCE:
293          (ix) FEATURE:
295          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
297 TAAATTTAAT TAATTCGGGC CCGTCGA 27
299 (2) INFORMATION FOR SEQ ID NO: 9:
301          (i) SEQUENCE CHARACTERISTICS:
302              (A) LENGTH: 69 base pairs
303              (B) TYPE: nucleic acid
304              (C) STRANDEDNESS: single
305              (D) TOPOLOGY: linear
307          (ii) MOLECULE TYPE: Genomic DNA
310          (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
312 ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT 48
313 Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu ←
W--> 315 GTC ACA AAC AGT GCA CCT ACT 69
316 Val Thr Asn Ser Ala Pro Thr ←

```

*number the
amino acids*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/724,693A

DATE: 02/06/2001

TIME: 16:04:48

Input Set : A:\402gseq.002

Output Set: N:\CRF3\02062001\I724693A.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
 L:9 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
 L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
 L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
 L:37 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
 L:42 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
 L:47 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
 L:73 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:78 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=1, Value=[]
 L:74 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=1, Value=[]
 L:113 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:118 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=2, Value=[]
 L:114 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=2, Value=[]
 L:151 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:156 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=3, Value=[]
 L:152 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=3, Value=[]
 L:211 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:216 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=4, Value=[]
 L:212 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=4, Value=[]
 L:230 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:235 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=5, Value=[]
 L:231 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=5, Value=[]
 L:249 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:254 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=6, Value=[]
 L:247 M:246 W: Invalid value of Alpha Sequence Header Field, [MOLECULE TYPE:], SeqNo=6, Value=[DNA]
 L:250 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=6, Value=[]
 L:270 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:275 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=7, Value=[]
 L:271 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=7, Value=[]
 L:290 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:295 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=8, Value=[]
 L:291 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=8, Value=[]
 L:308 M:220 C: Keyword misspelled or invalid format, [(D) OTHER INFORMATION:]
 L:308 M:220 C: Keyword misspelled or invalid format, Poss data loss, Seq 9, (D) OTHER INFORMATION:
 L:315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9
 L:339 M:220 C: Keyword misspelled or invalid format, [(H) DOCUMENT NUMBER:]
 L:433 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:438 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=11, Value=[]
 L:434 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=11, Value=[]
 L:452 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:457 M:246 W: Invalid value of Alpha Sequence Header Field, [FEATURE:], SeqNo=12, Value=[]
 L:453 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=12, Value=[]
 L:471 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:472 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=13, Value=[]
 L:512 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:513 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=14, Value=[]
 L:553 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:554 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=15, Value=[]

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L:593 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:594 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=16, Value=[]
 L:979 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:980 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=17, Value=[]
 L:1713 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1714 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=18, Value=[]
 L:1734 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1735 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=19, Value=[]
 L:1764 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1765 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=20, Value=[]
 L:1789 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1790 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=21, Value=[]
 L:1813 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1814 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=22, Value=[]
 L:1837 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1838 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=23, Value=[]
 L:1866 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1867 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=24, Value=[]
 L:1896 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1897 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=25, Value=[]
 L:1914 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1915 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=26, Value=[]
 L:1932 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1933 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=27, Value=[]
 L:1950 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1951 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=28, Value=[]
 L:1968 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1969 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=29, Value=[]
 L:1987 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:1988 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=30, Value=[]
 L:2005 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:2006 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=31, Value=[]
 L:2023 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:2024 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=32, Value=[]
 L:2041 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:2042 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=33, Value=[]
 L:2059 M:220 C: Keyword misspelled or invalid format, [(iv) ANTI-SENSE:]
 L:2060 M:246 W: Invalid value of Alpha Sequence Header Field, [FRAGMENT TYPE:], SeqNo=34, Value=[]